

GenCore version 5.1.4_p5-4578
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OM nucleic - nucleic search, using sw model

Run on:

April 15, 2003, 00:14:43 ; Search time: 368.413 seconds

(without alignments) 1,0012.591 Million cell updates/sec

Title:

US-09-001-737-7_COPY_15_1652

Perfect score:

1638

Sequence:

1 ATGGCAAAGAAATCAATT.....TGGGNGGATGGCGGATAA 1638

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters:

4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1980.DAT:*

2: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1981.DAT:*

3: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1982.DAT:*

4: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1983.DAT:*

5: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1984.DAT:*

6: /SIDS2/gcdata/geneseq/geneseq-emb1/NA1985.DAT:*

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21: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2001A.DAT:*

22: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2001B.DAT:*

23: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2002.DAT:*

24: /SIDS2/gcdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1038	100.0	1661	20	AXX86155
2	1620.2	98.9	1635	24	ABM69160
3	1433.4	86.3	2683	22	ABM56861
4	1140.4	69.6	1306	22	ABM56855
5	1122.6	68.5	1305	22	ABM69159
6	1062.4	64.9	1620	24	ABM69157
7	1062.4	64.9	215561	24	ABM71527
8	1039.2	63.4	1633	22	ABM90800
9	1038.4	63.4	1926	22	AAF25036

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1	
ID	AXX86155
XX	AXX86155 standard; DNA; 1661 BP.
AC	AXX86155;
XX	
DT	22-SEP-1999 (first entry)
XX	
DE	DNA encoding a Streptococcus pyogenes heat shock protein (Hsp60-2.
XX	
KW	Heat shock protein; Hsp60-2; immune response; immunological carrier;
KW	cancer control; tumour; sarcoma; cancer; gene therapy; ss.
OS	Streptococcus pyogenes.
XX	
PN	W09935270-A1.
XX	
PD	15-JUL-1999.
XX	
PF	29-DEC-1998; 98WO-CA01203.
XX	
PR	31-DEC-1997; 97US-0001737.
XX	
PA	(STRE) STRESSEN BIOTECHNOLOGIES CORP.
XX	
PI	Mizzen L, Wisniewski J;
XX	
DR	WPI: 1999-430397/36.
DR	P-PSDB; RAY21904.
XX	
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer

agents and for diagnosis

PT

XX

PS

XX

Claim 3; FIG 4A-B; 176pp; English.

The present sequence encodes a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elicit or enhance an immune response against *Streptococcus*, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting *streptococci* in standard hybridization/amplication assays, and therapeutically in gene therapy vectors.

SQ Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;

Query Match 100 %; Score 1638; DB 20; Length 1661;

Best Local Similarity 100 %; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 ATGGGAAAGAAATCAAAATTTCAGCAGATGCGCGTGCATGGCGGACTGTG 60

Db 15 ATGGGAAAGAAATCAAAATTTCAGCAGATGCGCGTGCATGGCGGACTGTG 74

QY

61 ATGGTAGCAGATCACCTCAAGAACTGACCTCTGGTCTAAAGGCGCAATGTG 120

Db 75 ATGGTAGCAGATCACCTCAAGAACTGACCTCTGGTCTAAAGGCGCAATGTG 134

QY

121 AAAGCTTGGTCTCCCTTAATCTAATGACGGGAAACATGGCTGAGTGCTAA 180

Db 135 AAAGCTTGGTCTCCCTTAATCTAATGACGGGAAACATGGCTGAGTGCTAA 194

QY

181 TTAGAGATCATTTGAAACATGGGCAAAATTGGTGTCTGAGTGCTCTAACACC 240

Db 195 TTAGAGATCATTTGAAACATGGGCAAAATTGGTGTCTGAGTGCTCTAACACC 254

QY

241 ATGGATATGCGGTCATGGGCAACTGCACTTGTACGCCAGCCATGTTG 300

Db 255 ATGGATATGCGGTCATGGGCAACTGCACTTGTACGCCAGCCATGTTG 314

QY

301 GAGGACTAAATGAGCAGCAAGCTTGTACGCCAGCCATGTTG 360

Db 315 GAGGACTAAATGAGCAGCAAGCTTGTACGCCAGCCATGTTG 374

QY

361 ACAGGAAACAGCAAACTCTTGTACGCCAGCCATGTTG 420

Db 375 ACAGGAAACAGCAAACTCTTGTACGCCAGCCATGTTG 434

QY

421 GAGSTATGCTCAGTCGCTGCGATCATCACGGCTGTGAAAGTTGGAGATATC 480

Db 435 GAGCTATGCTCAGTCGCTGCGATCATCACGGCTGTGAAAGTTGGAGATATC 494

QY

481 TCGAGGATATGAGCAGCTTGTACGCCAGCCATGTTG 540

Db 495 TCGAGGATATGAGCAGCTTGTACGCCAGCCATGTTG 554

QY

541 ATGGAAACAGAACTGAACTGAGTGGGCACTTGTACGCCATGTTG 600

Db 555 ATGGAAACAGAACTGAACTGAGTGGGCACTTGTACGCCATGTTG 614

QY

601 TACAGGCTCACAGACATGAAATGTTGCAACGACCTTGTACGCCATGTTG 660

Db 615 TACAGGCTCACAGACATGAAATGTTGCAACGACCTTGTACGCCATGTTG 674

QY

661 AGGGATAAAAGTGTCAACATCAGACATTTGCACTACTGTGAGTCTTAA 720

Db 675 AGGGATAAAAGTGTCAACATCAGACATTTGCACTACTGTGAGTCTTAA 734

QY

721 ACCAACCTCCATTACTCTATTGCGATGATGATGATGATGAACTTCACCCCT 780

Db 735 ACCAACCTCCATTACTCTATTGCGATGATGATGATGATGAACTTCACCCCT 794

QY

781 GTCTTGACAGAGATGCGTACTTTCATGATGATGATGATGATGATGCTGTC 840

Db 795 GTCTTGACAGAGATGCGTACTTTCATGATGATGATGATGATGATGCTGTC 854

QY

841 GATGCTGTTAAAGCTATGTTGAGACATGCTATGCTATGCTGATGCTGCTG 900

Db 855 GATGCTGTTAAAGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 914

QY

901 GAGGATCAGACTGAACTGAAAGTGTACATGACACCCCTGACAGGTGCTAG 960

Db 915 GAGGATCAGACTGAACTGAAAGTGTACATGACACCCCTGACAGGTGCTAG 974

QY

961 ATTACAGTTGAAAGAATGACAGCACTAATGTTGAGGGTCGGAGTCAGAGCTT 1020

Db 975 ATTACAGTTGAAAGAATGACAGCACTAATGTTGAGGGTCGGAGTCAGAGCTT 1034

QY

1021 GCTAACCTATGAGCTATTAATGCAATTGAAACACACTCTGACTTGACCGT 1080

Db 1035 GCTAACCTATGAGCTATTAATGCAATTGAAACACACTCTGACTTGACCGT 1094

QY

1081 GAAACTTACAGAACTGTTGGGAATATTGCTGGTGGTGGTGGTGGTGGTGGT 1140

Db 1095 GAAAACTTACAGAACTGTTGGGAATATTGCTGGTGGTGGTGGTGGTGGTGGT 1154

QY

1141 GCTCCAAACAGAGACGCTTAAAGAATGAAACTCCGATGCTGATGCTGCT 1200

Db 1155 GCTCCAAACAGAGACGCTTAAAGAATGAAACTCCGATGCTGCT 1214

QY

1201 ACAGCTGCGCCGTTGAGAAGGTTGCTGTGCTGCTGCTGCTGCTGCTGCT 1260

Db 1215 ACAGCTGCGCCGTTGAGAAGGTTGCTGTGCTGCTGCTGCTGCTGCTGCT 1274

QY

1261 ATGAAACAAAGAGACGCTTAAAGAATGAAACTCCGATGCTGATGCTGATG 1320

Db 1275 ATGAAACAAAGAGACGCTTAAAGAATGAAACTCCGATGCTGATGCTGATG 1334

QY

1321 CTGCGCTCTAGAGACGCCGCTGAGTGTAAATGCTTTAATGCTGCTGCTGCT 1380

Db 1335 CTGCGCTCTAGAGACGCCGCTGAGTGTAAATGCTTTAATGCTGCTGCTGCT 1394

QY

1381 GTAGTTGACAGTGTGAAACACGCCCTGCGAGCGAGGTTATGCTGCAACAGT 1440

Db 1395 GTAGTTGACAGTGTGAAACACGCCCTGCGAGCGAGGTTATGCTGCAACAGT 1454

QY

1441 GATGGTGTGATGATGAAACAGGAACTGCTGAGCTGCTGAGCTGCTGAGCTG 1500

Db 1455 GATGGTGTGATGATGAAACAGGAACTGCTGAGCTGCTGAGCTGCTGAGCTG 1514

QY

1501 CTGCAATGACAGCTGAGTGTGAAACAGGAACTGCTGAGCTGCTGAGCTG 1560

Db 1515 CTGCAATGACAGCTGAGTGTGAAACAGGAACTGCTGAGCTGCTGAGCTG 1574

QY

1561 AACCTGACAGCTGAGTGTGAAACAGGAACTGCTGAGCTGCTGAGCTG 1620

Db 1575 AACCTGACAGCTGAGTGTGAAACAGGAACTGCTGAGCTGCTGAGCTG 1634

RESULT 2

ABN69160

ID ABN69160 standard; DNA; 1635 BP.

XX

AC ABN69160;

XX

DT 01-JUL-2002 (first entry)

inhibiting expression of GL or GS in cells or tissues *in vitro*. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism, (I), (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AHN5652 to AHN5367 and AHN5633 to AHN5684 represent PCR primers for grot sequences which are used in the exemplification of present invention. AHN5685 to AHN5687 represent gross nucleotide sequence given in the present invention.

OY	247	ATGCTGGATGGAGACTACTGACACAGTTGACACAGCCATGTCATAGAGA	306
Db	61	ATPGCTGGATGGAGACTACTGACACAGTTGACACAGCCATGTCATAGAGA	120
OY	307	CTAAAGATGTACACAGCAGGTTAATCCATGATCCGTGACAGCCATGTCATAGAGA	366
Db	121	CTAAAGATGTACACAGCAGGTTAATCCATGATCCGTGACAGCCATGTCATAGAGA	180
OY	367	ACAGACAGCAGCTGGTGAACGCTCTGAAAGCCATTCTCACCTGATCGGGAGGCT	426
Db	181	ACAGACAGCAGCTGGTGAACGCTCTGAAAGCCATTCTCACCTGATCGGGAGGCT	240
OY	427	ATTCATGGTACGGTGCAGTACATCACTACGCTCTGAAAGTGGAGACTATATCAGA	485
Db	241	ATTCATGGTACGGTGCAGTACATCACTACGCTCTGAAAGTGGAGACTATATCAGA	300
OY	487	CTATGGAGCTGGTGAACGCTCTGAAAGTGGAGACTATATCAGA	546
Db	301	CTATGGAGCTGGTGAACGCTCTGAAAGTGGAGACTATATCAGA	360
OY	547	ACAGACTTGAGTGTGTTGACGCTGCTGTTACCTGCTCTCAATCATG	606
Db	361	ACAGACTTGAGTGTGTTGACGCTGCTGTTACCTGCTCTCAATCATG	420
OY	607	GTACAGACATGAAAAATGGTGGAGACCTGAAACCCATTATCTTATACGGAT	666
Db	421	GTACAGACATGAAAAATGGTGGAGACCTGAAACCCATTATCTTATACGGAT	480
OY	667	AAAAGACTGTCACATCCAGCTTGGCAACTCTGGGGAGTCTAAACACAC	726
Db	481	AAAAGACTGTCACATCCAGCTTGGCAACTCTGGGGAGTCTAAACACAC	540
OY	727	CGTCATACTATATTGACAGTATGGGGAGACCTTCAACCTTGCTG	786
Db	541	CGTCATACTATATTGACAGTATGGGGAGACCTTCAACCTTGCTG	600
OY	787	ACAGAGTCGGTACTTCATGGCTGCTTAAGGCCAGATTTGGGAGCT	846
Db	601	ACAGAGTCGGTACTTCATGGCTGCTTAAGGCCAGATTTGGGAGCT	660
OY	847	CGTAACGCTATGCTGAACATCTCATCTGACAGGGCTGCTACATGATTACAGAGAT	906
Db	661	CGTAACGCTATGCTGAACATCTCATCTGACAGGGCTGCTACATGATTACAGAGAT	720
OY	907	CTGAGCTGTGATTAAGATGCTCAATGAGAGCCCTGGACAGGGTGTAGATACA	966

Db	721 CTAGGACTGATTAAAGATGTTACATGACAGCCCTGGACAGCTGCTAAGATACA	780	PA (GENE-) GENESENSE TECHNOLOGIES INC.
OY	967 GTTGTAAAGATGACAGCACTAAATGTTGAAAGGTCAGACTTGAAAGCTTAC	1026	XX
Db	781 GTTGTAAAGATGACAGCACTAAATGTTGAAAGGTCAGACTTGAAAGCTTAC	840	PI Wright JA, Young AH, Dugourd D;
OY	1027 CTATGCACTATTAAATGCAATTAGAACACAACTCTGACTTGACCGTAA	1086	XX DR WPI; 2001-35633/37.
Db	841 CCATGCACTATTAAATGCAATTAGAACACAACTCTGACTTGACCGTAA	900	PT Novel antisense compounds targeting nucleic acid encoding groE or
OY	1087 CTACAGAGACGTTGGCAATTAGCTGGTGTAGCTGTTAAAGTGGACTCA	900	PT expression of the genes, useful to inhibit growth of microorganism
Db	901 CTACAGAGACGTTGGCAATTAGCTGGTGTAGCTGTTAAAGTGGACTCA	960	PT having the genes
OY	1147 ACAGAGACGCTTAAGAAGAACTCGCATAGGAGCTTAATGCTACAGT	960	XX Disclosure: Fig 8; 110pp; English.
Db	961 ACAGAGACGCTTAAGAAGAACTCGCATAGGAGCTTAATGCTACAGT	1206	CC The present invention specifically claims AAH56368 to AAH56832 which are
OY	1207 GCAGCGTGTAGAAGGATCTGGTGTAGCTGTTAAAGTGGACTCA	1146	CC antisense oligonucleotides to nucleotide sequences encoding groE. More
Db	1021 GCAGCGTGTAGAAGGATCTGGTGTAGCTGTTAAAGTGGACTCA	960	CC generally, antisense compounds (I) comprising antisense oligonucleotides
OY	1327 GCTCTAGAGAGCCCTGAGCTTAAACAGGATCTGGCTGCAAGTAC	1080	CC of 5-50 bases targeted to a nucleotide sequence encoding groE (heat
Db	1367 AAAGTGGAGCTCTGAGCTTAAAGAAGAACTTCGAGGCTTAATG	1206	CC shock protein (HSP10) (S1) and groS (HSP10) (GS) gene from a
OY	1081 AAATGAGCTGCTCTGAGCTTAAAGAAGAACTTACGGTTAA	1266	CC microorganism, where the antisense compound is complementary to GL or
Db	1261 GTTGTATGTTAAACAGGATCTGGTGTAGCTGTTAAAGTGGACTCA	1260	CC GS of a microorganism and specifically hybridises with and inhibits the
OY	1447 GTGATGATGATTAACAGGATCTGGCTGCAAGTACAGGATCTGGCT	1506	CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
Db	1441 GCTCTAGAGGCTTAAACAGGATCTGGCTGCAAGTACAGGATCTGGCT	1200	CC and antiproliferative activities, and can be used in antisense therapy
OY	1387 ATGACAGTGTAAACAGCCTGGAGAACAGGTTATCTCAAGGTTAG	1446	CC for inhibition of expression of groS or groE. (I) are useful for
Db	1201 ATGACAGTGTAAACAGCCTGGAGAACAGGTTATCTCAAGGTTAG	1260	CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
OY	1507 ATGCCAGCTCTGAGCTTAAACAGGATCTGGTGTAGCTGTTAAAC	1506	CC also useful for inhibiting the growth of a microorganism or inhibiting
Db	1321 ATGACGCTCTGAGCTTAAACAGGATCTGGTGTAGCTGTTAAAC	1566	CC the expression of GL or GS gene in a microorganism (a bacterial cell or
OY	1567 GACCACTAGGCCAGCAGCTGAGCTTAAACAGGATCTGGTGTAG	1625	CC a virus) having a GL or GS gene which involves administering to the
Db	1381 GAACCACTGCGCCAGGCCAGTATGACCTCAGGATGATGGGG	1439	CC microorganism or to a cell infected with the microorganism. (I) (I) are
RESULT 4			
ID	AAH56862 standard; DNA: 1306 BP.		CC also useful for treating a mammalian pathological condition mediated by
AC	AAH56862;		CC having a pathological condition mediated by a eukaryotic organism
XX			CC or GS gene and administering (I) such that the growth of microorganism
DT	05-SEP-2001 (first entry)		CC is inhibited. The antisense compounds are utilised for diagnostics
XX			CC and therapeutics, prophylaxis and as research reagents and kits, e.g., to
DE	Antibiotic resistant S. pyogenes groEL gene partial sequence SEQ ID:8.		CC prevent or delay microbial infections in humans. They are also useful as
XX	Antisense oligonucleotide; groE; groES; inhibitor; growth;		CC molecular weight markers. AAH56362 to AAH56367 and AAH5633 to AAH56854
KW	microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;		CC represent PCR primers for groE sequences which are used in the
KW	Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;		CC exemplification of the present invention. AAH56835 to AAH56870 represent
KW	antibacterial; antiviral; antiproliferative; antisense therapy;		CC groE nucleotide sequence given in the present invention.
XX	microbial infection; ds;		XX Sequence 1306 BP; 407 A; 235 C; 308 G; 356 T; 0 other:
Query Match			
Best Local Similarity 69.6%; Score 110.4; DB 22; Length 1306;			
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
OY	484 GAACTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG	543	QY 484 GAACTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG
Db	2 GAAGCTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG	61	Db 2 GAAGCTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG
OY	544 GAACTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG	603	QY 544 GAACTATGGACGGTGGGCACGATGGTGTGATTCATCGAGATCCTGGATG
Db	62 GAAACAGACTGGATGCTTAAAGCATGGTGTGATTCATCGAGATCCTGGATG	121	Db 62 GAAACAGACTGGATGCTTAAAGCATGGTGTGATTCATCGAGATCCTGGATG
OY	604 ATGGCTACAGACGAAATGGTGGAGCTTGAAACCAATTACTTAACT	663	QY 604 ATGGCTACAGACGAAATGGTGGAGCTTGAAACCAATTACTTAACT
Db	122 ATGGCTACAGACGAAATGGTGGAGCTTGAAACCAATTACTTAACT	181	Db 122 ATGGCTACAGACGAAATGGTGGAGCTTGAAACCAATTACTTAACT
OY	664 GATAAAAGTCAACATCCAGACATTGCGACTACTTGAGGAGTCCTAA	723	QY 664 GATAAAAGTCAACATCCAGACATTGCGACTACTTGAGGAGTCCTAA
Db	182 GATAAAAGTCAACATCCAGACATTGCGACTACTTGAGGAGTCCTAA	241	Db 182 GATAAAAGTCAACATCCAGACATTGCGACTACTTGAGGAGTCCTAA
OY	724 AACGGTCCATTACTCATTTACAGATGTTGAGGTTGAGCACTTCACCC	783	QY 724 AACGGTCCATTACTCATTTACAGATGTTGAGGTTGAGCACTTCACCC
Db	242 AACGGTCCATTACTCATTTACAGATGTTGAGGTTGAGCACTTCACCC	301	Db 242 AACGGTCCATTACTCATTTACAGATGTTGAGGTTGAGCACTTCACCC
OY	784 TTGACAGATTCGGTCACTTCAGATGGTGTGCGTAAAGGCCAGATTGGAT	843	QY 784 TTGACAGATTCGGTCACTTCAGATGGTGTGCGTAAAGGCCAGATTGGAT
Db	302 TTGACAGATTCGGTCACTTCAGATGGTGTGCGTAAAGGCCAGATTGGAT	903	Db 302 TTGACAGATTCGGTCACTTCAGATGGTGTGCGTAAAGGCCAGATTGGAT
OY	844 CGCGTAACTATGCTGAGACATGCTCTGAGGGGGTACAGTACAGAG	903	QY 844 CGCGTAACTATGCTGAGACATGCTCTGAGGGGGTACAGTACAGAG
Db	362 CGTCGAAGCTGAGCATGCTACTGAGCATGGTACAGTACAGAG	421	Db 362 CGTCGAAGCTGAGCATGCTACTGAGCATGGTACAGTACAGAG

QY	904	GATCTAGACTGATTAAGATAGCTACATGACAGCCTTGACAGGCTGTAAGATT	963	XX	PD	25-MAY-2001.
Db	422	GATCTAGACTGATTAAGATAGCTACATGACAGCCTTGACAGGCTGTAAGATT	481	XX	PF	20-NOV-2000; 2000WO-CA01347.
QY	964	ACAGTTGATAGATAGACAGTATGTTGAGGTCAGGAGTCAGAGCTAGATT	1023	XX	PR	18-NOV-1999; 99US-016249.
Db	482	ACAGTTGATAGATAGACAGTATGTTGAGGTCAGGAGTCAGAGCTAGATT	541	XX	PA	(GENE-) GENESENSE TECHNOLOGIES INC.
QY	1024	ACCGATTCACGATGATAATCCAAATTAGAACACACTCTGACTTGACGGTA	1083	PT	Wright JA, Young AH, Dugourd D;	
Db	542	ACCGATTCACGATGATAATCCAAATTAGAACACACTCTGACTTGACGGTA	601	DR	WPI: 2001-355633/37.	
Db	662	CCACAGAGACACTTAAAGAAATGAAACTTCACATGAGGAGTCCTAAATGCA	721	XX		
QY	1204	CTTGAGCCCTTGTAGAGGATGTTGCTGTTGGACAGCACTTTAGGTT	1143	XX	PT	Novel antisense compounds targeting nucleic acid encoding groEL or
Db	602	AACTACAGAAAGGTTGGCAATTAGCTGTTGTTGAGCTTAACTGAGCT	661	CC	PT	novel antisense compounds targeting nucleic acid encoding groEL or
QY	1144	CCACAGAGACACTTAAAGAAATGAAACTTCACATGAGGAGTCCTAAATGCA	1203	CC	PT	expression of the genes, useful to inhibit growth of microorganism
Db	782	GGAAAGTGTACCTTGAGCTGAGCTGAGCTGAGGCGATGTGAGGATC	1323	CC	PT	having the genes.
QY	1264	GGAAAGTGTACCTTGAGCTGAGCTGAGCTGAGGCGATGTGAGGATC	1323	CC	PS	Disclosure: Fig 11; 110P; English.
Db	782	GGAAAGTGTACCTTGAGCTGAGCTGAGCTGAGGCGATGTGAGGATC	1323	CC		
QY	1324	CTGGCTCTAGAACAGCTGACGCAATGCTTAATGCGGTACAAAGCCTG	1383	CC		
Db	842	CTGGCTCTAGAACAGCTGACGCAATGCTTAATGCGGTACAAAGCCTG	901	CC		
QY	1384	GTATGACAGTGTAAACAGGAGCATGACCCGTGAAAGTAAACGGCT	1443	CC		
Db	902	GTATGACAGTGTAAACAGGAGCATGACCCGTGAAAGTAAACGGCT	961	CC		
QY	1444	TCGGTGTATGTTAAACAGGAGCATGACCCGTGAAAGTAAACGGCT	1503	CC		
Db	962	TCGGTGTATGTTAAACAGGAGCATGACCCGTGAAAGTAAACGGCT	1021	CC		
QY	1504	CAAAATGAGCTCTATCTACTTTGAAACAGAGCGCTGTTGCTATAAA	1563	CC		
Db	1022	CAAAATGAGCTCTATCTACTTTGAAACAGAGCGCTGTTGCTATAAA	1081	CC		
QY	1564	CTTGACCAAGCTACSCACSGCCGACATGCCACAGCTGTTGAGTGTG	1623	CC		
Db	1082	CTTGACCAAGCTACSCACSGCCGACATGCCACAGCTGTTGAGTGTG	1141	CC		
QY	1624	GG 1625		XX		
Db	1142	GG 1143				
RESULT 5						
AAH5685						
XX						
AC						
AAH56865;						
XX						
06-SEP-2001 (first entry)						
XX						
Antibiotic resistant S. pyogenes groEL gene partial sequence SEQ ID:11.						
XX						
Antisense oligonucleotide; groEL; groES; inhibitor; growth;						
XX						
microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;						
XX						
Streptococcus progenes; Staphylococcus aureus; Pseudomonas aeruginosa;						
XX						
antibacterial; antibiotic; antiproliferative; antisense therapy; ds;						
XX						
Streptococcus Progenes.						
XX						
W0200136625-A2.						

QY	361	ACGACACAGCACACAGCTGTTGAGGCCATGCTCACCTGATCGCAG 420	Db	1441	GAATGGTAGATGGTACACAGGATCATGGACGCCAACCTTGCA 1500
Db	361	ACACGTTTCAAGGAGCTGAGCTTAAAGAGATGACAGCTTACCGAA 420	QY	421	GAAGCTTATGCTCGAGGAGTGGAGCTTAAAGAGATGACAGCTTACCGAA 480
Db	421	GAAGCTTATGCTCGAGGAGTGGAGCTTAAAGAGATGACAGCTTACCGAA 480	Db	481	TCTGAGCTATGCTGAGCTGCGCTGGTGGTATGCTGAGCTTACCGAA 540
Db	481	TCTGAGCTATGCTGAGCTGCGCTGGTGGTATGCTGAGCTTACCGAA 540	QY	541	ATGGAGACAGACTGTGAGTGGTGAAGGAGCTTACCGAA 600
QY	541	ATGGAGACAGACTGTGAGTGGTGAAGGAGCTTACCGAA 600	Db	541	ATGGAGACAGACTGTGAGTGGTGAAGGAGCTTACCGAA 600
QY	601	TACATGGTCAAGACAGCAATGAAATGTTGACGACTTACCGAA 660	Db	601	TATATGGTAACTCTAAACGAGAAATGGTCTCTGACTTGAGATCGGTATCTTATT 660
Db	601	TATATGGTAACTCTAAACGAGAAATGGTCTCTGACTTGAGATCGGTATCTTATT 660	QY	661	AGGAGTAAAGTCAAGACAGCAATGAAATGTTGACGACTTACCGAA 720
QY	661	AGGAGTAAAGTCAAGACAGCAATGAAATGTTGACGACTTACCGAA 720	Db	661	ACGATAGTAAAGTCAAGACAGCAATGAAATGTTGACGACTTACCGAA 720
Db	721	ACCAACCGTCAAACTCATATGCAAGATGAGATTTGGATGGTGGTACAGT 780	QY	721	ACCAACCGTCAAACTCATATGCAAGATGAGATTTGGATGGTGGTACAGT 780
Db	721	ACCAACCGTCAAACTCATATGCAAGATGAGATTTGGATGGTGGTACAGT 780	QY	781	GTCTGCAAGAAGATGTTGTTACATGAAATGTTGACGACTTACCGAA 840
Db	781	GTCTGCAAGAAGATGTTGTTACATGAAATGTTGACGACTTACCGAA 840	QY	841	GTATCTCGAAAGCTATGCTGAGACATCTCTGACGGTGTACAGTATACA 900
Db	841	GTATCTCGAAAGCTATGCTGAGACATCTCTGACGGTGTACAGTATACA 900	QY	901	GAGGTCTGGTGGTGTAGCTTAAAGATGCTAACATGACAGCCTGGACAGCTGTAG 960
Db	901	GAGACCTGGTGTAGCTTAAAGATGCTAACATGACAGCCTGGACAGCTGTAG 960	QY	961	ATTTACAGTGTGAAATACAGATGTTAGTTGGAGTCAGAACTTA 1020
Db	961	ATTTACAGTGTGAAATACAGATGTTAGTTGGAGTCAGAACTTA 1020	QY	1021	GCTAACCGTATTGCACTGTTAAATGCCATTAGAACGACAGCTCTGGCTGGGAGCTCATGGAA 1080
Db	1021	GCTAACCGTATTGCACTGTTAAATGCCATTAGAACGACAGCTCTGGCTGGGAGCTCATGGAA 1080	QY	1081	GAATAACTCAGAACGACTTGTGTTAGTGGCGGTGTAGCTTAAAGTAA 1140
Db	1081	GAATAACTCAGAACGACTTGTGTTAGTGGCGGTGTAGCTTAAAGTAA 1140	QY	1141	GCTCCAAAGACAGACGCTTAAAGAAATTAACCTCCATGAGGACTCTAAAGT 1200
Db	1141	GCTCCAAAGACAGACGCTTAAAGAAATTAACCTCCATGAGGACTCTAAAGT 1200	QY	1141	CGACGACTGAAAGATTAACCTCCATGAGGACTCTAAAGT 1200
Db	1141	CGACGACTGAAAGATTAACCTCCATGAGGACTCTAAAGT 1200	QY	1201	ACAGCTGAGGCTGTAAGAGTGTGCTGCTGCTGAAAGCCTTAAAGCT 1260
Db	1201	ACAGCTGAGGCTGCTGAAAGCCTTAAAGCT 1260	QY	1201	ACGGCTGCTGCTGAAAGCCTTAAAGCT 1260
Db	1201	ACGGCTGCTGCTGAAAGCCTTAAAGCT 1260	QY	1261	ATGGAAAGATGCGACTTGTGAGGGAGATGCTACTGGAGTACATGTC 1320
Db	1261	ATGGAAAGATGCGACTTGTGAGGGAGATGCTACTGGAGTACATGTC 1320	QY	1261	ATGGAAAGATGCGACTTGTGAGGGAGATGCTACTGGAGTACATGTC 1320
Db	1261	ATGGAAAGATGCGACTTGTGAGGGAGATGCTACTGGAGTACATGTC 1320	QY	1321	CTGGTGTCTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380
Db	1321	CTGGTGTCTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380	QY	1381	CTAGTGTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380
Db	1381	CTAGTGTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380	QY	1381	CTAGTGTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380
Db	1381	CTAGTGTGAAAGAGCTGACCTCAATGCTTAATGGTGTACAGATGTC 1380	QY	1441	GACGGGGTGTAGTAAACAGGAATCATGGACCTGTGCAAGTACAGATCGGG 1500

PT
XX
resistant bacterial infections -

The present invention relates to nucleic acids (AMH9071-AAH90918) encoding polypeptides (AAW01002-AAW0114), which are essential for the viability of a bacterial cell wall. The acronym CEG stands for "CEG For Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleic sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon by integrating an exogenous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of target suitable for the treatment of antibiotic resistant bacterial infections.

xx SQ Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;

Query Match 53.4%; Score 1038; DB 20; Length 1654;

Best Local Similarity 77.5%; Pred. No. 1.4e-61;

Matches 1257; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

xx QY 1441 GACTGGCTGATGANTAAACAGGAGTCATGACCCGTGCAARAACTAACAGATAGCG 1380

Db 1381 ATCGTTATCGATCGTTGAAAAATGCTGAGCTGTGTTAGGATTCAACCGAACGGC 1440

QY 1441 GACTGGCTGATGANTAAACAGGAGTCATGACCCGTGCAARAACTAACAGATAGCG 1500

Db 1441 GACTGGTTTACAGTGTGAGTGTGAACTGATGTCAGTGTGTTAGGATTCAACCGAACGGC 1500

QY 1501 CTTCAAATTCACCTTGCTGCTGCTGAGCTGTGTTAGGATTCAACCGAACGGC 1560

Db 1501 CTTCAAATTCACCTTGCTGCTGCTGAGCTGTGTTAGGATTCAACCGAACGGC 1560

QY 1561 AACACGAGAACCTAGGCCGCCAGCAATGCCAGAGGATGATCCAGAATGAT 1620

Db 1561 AACACGAGAACCTAGGCCGCCAGCAATGCCAGAGGATGATCCAGAATGAT 1620

QY 1621 GGTG 1624

Db 1621 GGTG 1624

RESULT 10

AXX80153 ID AXA61133 standard; DNA; 1654 BP.

XX AXA61133;

XX 22-SEP-1999 (first entry)

XX DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.

XX Heat shock protein; Hsp60-2; immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.

XX Streptococcus pneumoniae.

OS W0935270-A1.

PN

XX 15-JUL-1999.

XX 29-DEC-1998; 98PO-CA01203.

XX 31-DEC-1997; 97US-0001737.

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PT Mizzen, L., Wisniewski, J.; WPT; 1999-430397736.

DR P-PSDB, RAY23902.

XX New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis

XX

PS Claim 3; FIG 2A-B; 17pp; English.

CC The present sequence encodes a heat shock protein, designated Hsp60-2. The protein, its fragments and fusion proteins are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplication assays, and therapeutically in gene therapy vectors.

xx SQ Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;

Query Match 53.4%; Score 1038; DB 20; Length 1654;

Best Local Similarity 77.5%; Pred. No. 1.4e-61;

Matches 1257; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

xx QY 1 ATGGCAAAAGAAATCAATTTTCAGAGAGGCGCGCTCCAGGCGGGAGCTAT 60

Db 15 ATGGCAAAAGAAATCAATTTTCAGAGAGGCGCGCTCCAGGCGGGAGCTAT 74

QY 61 ATGTTAGCAGATGCTCAAGTAAGCTGCTGTTAGGACAGACAGCAGTCGAA 120

Db 75 ATCCTGCGATGACTCTTAAGTAACTTGGACCTAAAGGGCCATGTGTTCTGAA 134

QY 121 AAAGCTTGTGTTGCTCCATTACTAATGAGGGTTAACCATGTTAAAGATGAA 180

Db 135 AAGTCATTCGGTCAACCTGTGATTAACGAACTGAGGGTGTGACTATGCAAAAGAAATGAA 194

QY 181 TTAGGAGTATGGAAACATGGGAGCAATGGTGTGTTGAGGGCTCTAAAC 240

Db 195 TTAGGAGTACCTTGGTAAATGGTGTGCAATTTGTGATGAA 254

QY 241 ATGATGATATGCGGGATGTTGAGCTGACAGCTGTTGACACAGCTGTCAT 300

Db 255 ATGTTACGGTGGATGAACTTACACTGACATGCTGTTGACAGCAATGTCAT 314

QY 301 GAAGGACTTAAATATGTCAGCAGGTGTTAATTCATTTGTTGTCCTCCAGCATGAA 360

Db 315 GAAGGAACTCAAAAGTCACAGCAGTCAGGTTGAAACAACTGAA 374

QY 361 ACAGGAAAGAACAGCTGTTGAGGGAGCTACTGACACGTTGACACAGCTGTCAT 420

Db 375 ACAGCAGCTGCGCAGCAGTGAATGTTGAAACAACTGATCCTCTGTTGCGAA 434

QY 421 GAACGTTATGCTCAGTGTCTCGCATGATCATCACGCTGAACTGAA 480

Db 435 GAGCTATGCTCAAGTGTCAAGCTGTTGAGCTATCTGTTGAGTACATC 494

QY 481 TCAAGAAGTGTGAGGCGCTGGCAACGGTGTGATACATGAGATTCGGGT 540

Db 495 TCTGAGGATGTGAGAAGTGTGCAAGAGGGTGTATCCTGAGGATGTCGTTG 554

QY 541 ATGGRAGAGACTTGAGTGTGTTGAGCTGTTGAGCTGAGCAATTGAA 600

Db 555 ATGGRAGAGCTTGAGTGTGAGCTGAGGATGAGTGTGTTGAGCTGTTGCAAA 614

QY 601 TACAGGGTACAGACATGAAATAGTGTGAGACCTGCTGAAACCCATTACTATTC 660

Db 615 TACATGGTACAGATGAGTGTGAAATAGTGTGAGCTGAGCTGTTGAGAAATCGTACATTGAT 674

QY 661 ACGGTAAAGAATGTCACAAATCCAAAGACATTTGCCACTTGTGTTGCTAA 720

Db 675 ACACACAGAAATTCCTAACATTCACAAACACTTGGAAAGCATTCACAA 734

QY 721 ACCACCCCTTACTCTACTATGAGCTGAGTGTGAGTGTGAGACCTCCACCC 780

Db 735 AGCATGTCACCTGTGATTCGGATGATGTTGAGCTGTTCCACTCTT 794

QY 781 GTCUTGACAAAGATGCGGACTTCATGGTGTGCTAACGCCAGGATTG 840

Db 795 GTTGTGACAGATGCTGGAGCTCAGTGTGAGCTGTTGTTGGT 854

QY 841 GATGTTGCTGAGTGTGAGCTGAGCTGAGCTGTTGAGCTGTTGAGCTGTTG 900

Db 855 GACCTGCGACAGCACTTGAGTGTGAGCTGTTGAGCTGTTGAGCTGTTG 914

QY 901 GAGGATCTGAGCTGAAATGAGTGTCTGAGACAGCCTGGAGCTGTGAG 960

Db 915 GAGGACCTGCTGAGTGTGAGTGTGAGCTGAGCTGTTGAGCTGTTG 974

QY 961 ATGACAGTGTAAAGATGAGCTGAGCTGTTGAGGTTGAGCTGAGCTGTTG 1020

QY 541 ATGGAACAGAACCTGAAAGTGGCTTAAGGCATGCAATTGACCGTGGTTACCTGTCCAA 600
 Db 541 ATGGAACAGAACCTGAAAGTGGCTTAAGGCATGCAATTGACCGTGGTTACCTGTCCAA 600
 QY 601 TACGGTCAAGAACGAAATGAAATGGTGGACCTTGAAACCAATTATTCATC 660
 Db 601 TACGGTCAAGAACGAAATGAAATGGTGGACCTTGAAACCAATTATTCATC 660
 QY 661 ATCGATAAAACGTCAAACCTCAGAACATTGCACTTGAACTTGAAATCGTAA 720
 Db 661 ATCGATAAAACGTCAAACCTCAGAACATTGCACTTGAACTTGAAATCGTAA 720
 QY 721 ACCAACCGTCCATACTCATPATCGAGATGATGATGAGTGGAAACACTCCACCT 780
 Db 721 ACCAACCGTCCATACTCATPATCGAGATGATGATGAGTGGAAACACTCCACCT 780
 QY 781 GTCUTGACAGATTCGNGTRACTTCATCTGTTGCTCAAAAGGAGATTGGT 840
 Db 781 GTCUTGACAGATTCGNGTRACTTCATCTGTTGCTCAAAAGGAGATTGGT 840
 QY 841 GATCGTGTAAAGCTATGCTGAGACATGATGTTGACAGGTGATCGTAA 900
 Db 841 GATCGTGTAAAGCTATGCTGAGACATGATGTTGACAGGTGATCGTAA 900
 QY 901 GACCGTGCAGAACGCGATCTGAGATGCGATCTGCACTTCAGCGGAGATTCAC 960
 Db 901 GACCGTGCAGAACGCGATCTGAGATGCGATCTGCACTTCAGCGGAGATTCAC 960
 QY 961 ATTACAGTGTAAAGATAGACGAGCTTAATGCTGAGACACCCGAGCTGAGCTT 1020
 Db 961 ATTACAGTGTAAAGATAGACGAGCTTAATGCTGAGACACCCGAGCTGAGCTT 1020
 QY 1021 GCTAACCGTATGCACTGATTAATGCAATTAGACACCAACTCTGACTTGACGT 1080
 Db 1021 TCTCACCGTGTGGGTATTAATGCAATTAGACACCAACTCTGACTTGACGT 1080
 QY 1081 GAAAACTAGAACGAGCGTTGGAAATTAGTGCGGTTGAGCTTAAAGTGA 1140
 Db 1081 GAAAACTAGAACGAGCGTTGGAAATTAGTGCGGTTGAGCTTAAAGTGA 1140
 QY 1141 GCTCCACAGAGAACCTTAAAGAACCTCGCATGAGTGTCTAAATGCT 1200
 Db 1141 GCGGCACTACTGAGTGTCTAAAGAACCTCGCATGAGTGTCTAAATGCT 1200
 QY 1201 ACACGGCAGCGCTGTGAGAGGAGTCCTGGGGGAGACACTATACGGT 1260
 Db 1201 ACACGGCAGCGCTGTGAGAGGAGTCCTGGGGGAGACACTATACGGT 1260
 QY 1261 ATTGAAAGAAGTAGACGAGCTCTGAGCTGAGGGCTGAGCTGAGCTA 1320
 Db 1261 ATTGAAAGAAGTAGACGAGCTCTGAGCTGAGGGCTGAGCTGAGCTA 1320
 QY 1321 CTTCGCTCTGAGACCTGAAATGCTGAAATGCTGAGGGCTC 1380
 Db 1321 CTTCGCTCTGAGACCTGAAATGCTGAAATGCTGAAATGCTGAGGGCTC 1380
 QY 1381 GAGTATTGACAGTGGAAAGAGCCCTGAGACAGGAAATTATGCACTGAGCT 1440
 Db 1381 GAGTATTGACAGTGGAAAGAGCCCTGAGACAGGAAATTATGCACTGAGCT 1440
 QY 1441 GAGTGGTGTAGTGTAAACAGGAACTGACCTGTCAGAACGATGAGCG 1500
 Db 1441 GAGTGGTGTAGTGTAAACAGGAACTGACCTGTCAGAACGATGAGCG 1500
 QY 1501 CTTCAAATGACGACTCTGAGCTGAGCTTATTTGACACAGACAGCTGTT 1560
 Db 1501 CTTCAAATGACGACTCTGAGCTGAGCTTATTTGACACAGACAGCTGTT 1560

RESULT 12
 AAH5660
 ID AAH5660 standard: DNA; 2107 BP.
 XX
 AC AAH5660;
 XX
 DT 05-SEP-2001 (first entry)
 DE Antibiotic resistant S. pneumoniae groE operon sequence SEQ ID NO:6.
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus Pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ds;
 OS streptococcus pneumoniae.
 XX
 PN WO200136625-A2.
 XX
 PT 25-MAY-2001.
 XX
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PR 18-NOV-1999; 9905-0166249.
 XX
 PI Wright JA, Young AH, Dugourd D;
 XX
 DR WPI; 2001-355633/37.
 XX
 PT Novel antisense compounds targeting nucleic acid encoding groEL or
 PT groES gene of microorganism, which hybridize with and inhibit
 PT expression of the genes, useful to inhibit growth of microorganism
 PT having the genes.
 XX
 PS Disclosure; Fig 6; 110pp; English.
 CC The present invention specifically claims AAH5638 to AAH5632 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groEL.
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL
 CC or GS gene and administering (I) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilised for diagnostic,
 CC therapeutic, prophylaxis and as research reagents and kits, e.g., to
 prevent or delay microbial infections in humans. They are also useful as
 molecular weight markers. AAH5636 to AAH5637 and AAH5683 to AAH5654
 CC represent PCR primers for groE sequences which are used in the
 exemplification of the present invention. AAH5655 to AAH5870 represent
 CC groE nucleotide sequence given in the present invention.
 XX
 Sequence 2107 BP; 650 A; 400 C; 508 G; 549 T; 0 other;
 Query Match 63.2%; Score 1036; DB 22; Length 2107;
 Best Local Similarity 77.5%; Pred. 0; Seq. 263; Mismatches 365; Indels 0; caps 0;
 Matches 1255; Conservative 0; Mismatches 365; Indels 0; caps 0;

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV2134 to AAV5224) recorded on it, or a representative fragment, at least 95% identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV2134 to AAV5224) are genomic fragments from *Streptococcus pneumoniae*. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the *S. pneumoniae* genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of *S. pneumoniae* genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the *S. pneumoniae* genome of commercial importance. Or expression modulating fragments of the *S. pneumoniae* genome products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for *S. pneumoniae*.

Best Local Similarity 77.4%; Pred. NO. 1.9e-260+; Length 3505; Matches 1254; Conservative 0; Mismatches 356; Index 0; Gaps 0;

278	ATGCTCAGAAGAATTAAATTTCATCAGATGCCCTTCAGCATGGTGTGGATGATGAT	Db	1358	GAAMAATGCAAGAACGCTGGCCAAATGTCAGGGTGTACGGTTAAAGTGTGA
61	ATTTAGCAGATGAGTCGTCAGAAGTAACTCTGGCTCAAGTAACTCTGGCTCTGAA	Qy	1441	GCTCAAAGAGAACGCTTAAKAGAATGAGAATGAGACTTGCAATAGGTTCTAATGT
338	ATCCTGAGCACACGTGTTAAGTGTACCTGGGACCAAGGTCGCAATGCTCTGAA	Db	1418	GCCTCAACTGAAACTGAGTGTGAAAGAAATGAACTCAGTTCAGTGGCTCCTAACGT
121	AAAGCTTGTGTCCTCTTAAATCTAATGACCTGACCGGGAAACCATGCTCTGAA	Qy	1201	ACAGTCAGCGGTGAGAGGTATGTTGAGAAGACAGACTTACCGTT
398	AATGCTGGTGTGACCTGAACTCTGATTCACAAATGCGTGGACCATGCCAAGATCGA	Db	1478	ACTGTGCGCTGAGAAGTGTGTTGGAGGTTGGGAGGAGACACTTACCGTT
181	TTAGAAGATCATTGAAACATGGGCAAAATTGGGCTGAGTGCTCTCAAAAC	Qy	1261	ATTTAAAGATGAGCAGCTTGAGCTTGAGTTGAGTCAACTATGT
458	TTGGAGAACATTTGAAATATGGGPGCTGAGTATGATAGAAGTGTCTAAAC	Db	1538	ATTCAGCTGTCTACCTTGGAAATGACAGGAGATGAGCAACAGGACTTAATGTT
241	AATGATATGCTGTTGACCTGAGGACACTACTGCAACAGTTTGACACAGCAATGTC	Qy	1321	CTTGCTCTCTAGAGAGGCGCTAGTCGAATGCTTTAACTCTGGTACGAGCTCC
517	ATGATATGCGAGTGACGAACTAGCTGACCTGAACTCTGACCCAGCTATCCTC	Db	1598	CTCCGCTTGGAGAACGCCGTTGGTCAATTGCAAGTACAGGATTGAGGATC
318	ATGATATGCGAGTGACGAACTAGCTGACCTGAACTCTGACCCAGCTATCCTC	Db	1538	ATTCAGCTGTCTACCTTGGAAATGACAGGAGATGAGCAACAGGACTTAATGTT
301	TTAGGACTTAAATGACGAGGTGCTATCCATTGCTATCCGGTGAGGATGAA	Qy	1381	GTAAATTGAGCAAGTGTGAAACACGCCCCTGCAATGCTTTAACTCTGGTACGAGCTCC
578	TTAGGACTTAAATGACGAGGTGCTATCCATTGCTATCCGGTGAGGATGAA	Db	1658	ATGCTTACGATCTTGGAAATGCTGTGAGCTTGCTGTTGATGATTACCGAGAACG
361	ACAGCAAAAGCAGACAGCTTGAGGCTTGAAAGCCATTGCTCACCTGTTGCGAG	Qy	1441	GAGGGGTGATGATTAACAGAGACATGACCTGCAACTAACGAGTACCG
638	ACAGCAAAAGCAGACAGCTTGAGGCTTGAAAGCCATTGCTCACCTGTTGCGAG	Db	1718	GASTGGTTAACATGATGATGACAGGATATCTGTTGAGTGTCTGAGC
421	GAAGTGTGCTGCAAGTCTGAGATCATCGCCCTGAAAGAATGGGAGAGATAC	Qy	1501	CTCAAAATTCAGCTCTGAGCTAGTCTTATTTGACACAGAGCAGTGTGTTAAT
698	GAAGTGTGCTGCAAGTCTGAGATCATCGCCCTGAAAGAATGGGAGAGATAC	Db	1778	CTCAAAATTCAGCTCTGAGCTAGTCTGAGCTGAGATGATCCAGGATGAT
481	TCAAGAGTGTGCTGAGCTGGCAACAGTGGTGTGTTACCATGAGAATCTGAGT	Qy	1561	AAACCTGACACGCTAGCCAGCAGTGGCTGAGTGTGTTGATGATGATGAT
758	TCTGAGCAATGAAAGTGGCAAGACGGCTCTCACCATCGAGAATGCTGAGT	Db	1838	AAACCAAGACAGTAGGCCCTCAGGATGATCCAAAGCATGATGGCAGACTG
541	ATGGAAAGACAGTCTGAGTGGTGAAGGATCAATTGACCTGGTACCTGTC	RESULT 14		
818	ATGGAAAGACAGTCTGAGTGGTGAAGGATCAATTGACCTGGTACCTGTC	AHH5659		
601	TACTGGCAGACAGAAATGGTGCAGACCTGAAACCCATTATCTAAAC	ID		
660		AAH56859;		
78	TACAGGGTACAGATAGCGAAAAATGGTGCCTGACCTTGTAAATCGTACATTGAT	XX		
937		06 - SEP - 2001 (first entry)		

DE XX S. pneumoniae groE operon nucleotide sequence SEQ ID NO:5.
 KW Antisense oligonucleotide; groE; groE; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; *Pseudomonas aeruginosa*;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ds.
 XX OS Streptococcus pneumoniae.
 XX PN WO200136625-A2.
 XX PD 25-MAY-2001.
 XX PF 20-NOV-2000; 2000HO-CH01347.
 XX PR 18-NOV-1999; 99US-0166249.
 XX PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX PI Wright JA, Young AH, Dugourd D;
 XX DR Wright JA, Young AH, Dugourd D;
 XX WPI: 2001-355633/37.
 PS Disclosure: FIG 5; 110pp; English.
 CC The present invention specifically claims AAH56368 to AAH56372 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE or
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groE (heat
 CC shock protein (HSP)60) (GL) and groS (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or
 CC GS of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral
 CC and antiproliferative activities, and can be used in antisense therapy
 CC and for inhibition of expression of groE or groS. (I) are useful for
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or
 CC a virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected by the microorganism. (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL
 CC or GS gene and administering (I) such that the growth of microorganism
 CC is inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 prevent or delay microbial infections in humans. They are also useful as
 molecular weight markers. AAH56362 to AAH56367 and AAH6833 to AAH5654
 exemplification of the present invention. AAH5655 to AAH56870 represent
 CC PCR primers for groE sequences which are used in the AAH5654
 CC exemplification of the present invention. AAH5655 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention.
 XX Sequence 2401 BP; 743 A; 459 C; 568 G; 631 T; 0 other;
 SQ Query Match 62.9%; Score 1039.5; DB 22; Length 2401;
 Best local Similarity 77.2%; Pred. No. 2.5e-259; Mismatches 369; Indels 0; Gaps 0; Matches 1251; Conservative 0; Mismatches 369; Indels 0; Gaps 0;
 Oy 1 ATGGCAAAAGAAATAAATTCTGAGCTAGGCGGCGCTCCATGGCGCCGTCACCGTCATGGTCTGGT 60
 Db 61 ATGGTAGGAGATACCGTCAACTAACGCTTGGCTCTAAGGGCGCATGTTGCTGAA 678
 Oy 61 ATGGTAGGAGATACCGTCAACTAACGCTTGGCTCTAAGGGCGCATGTTGCTGAA 678
 Db 679 ATCCCTGCGAGACGACTGTTAACCTGCTGGCCAAAGATGCCATGCGTCGTCTGAA 120
 Oy 679 ATCCCTGCGAGACGACTGTTAACCTGCTGGCCAAAGATGCCATGCGTCGTCTGAA 120
 121 AACGTTTGGTCTCCCTAACTAATGAGGGTACCTATCTAAGAGATGAA 180

Db	739	AAAGTCATGGGTCACCCGTTGATTAATGAGGTGTTGACCATGCGCAAGAAGATGAA
Qy	181	TTAGAGATCATTTGAAACAGGGGCAAAATTGGTGTGTTGAGGGCTCTAAACC
Db	799	TTGGAGACCATTTGAAATATGGGTGCTAATTGATCAGAAATGCTTAAACC
Qy	241	ATGGATATGGCTGTTGGAGGACTACTGCAACATTGACAGCAGATGTC
Db	859	ATGTATGATGCGAGGAGCGACTAGCTGCAACAGCTGTCAGTCTTACAGT
Qy	301	GAGGACTAAATGTCAGCAGGGTCTAATCAGTGTATGCAATGAGATGAA
Db	919	GGAGGATCAAAACCTCACAGAGCTGCAAGCTGAACTGGATGAA
Qy	361	ACAGCAACAGCACACGCTGTGAGCCTGAGCCATGCTCACCTGTCAG
Db	979	ACAGCAGTGGCGCACAGTGAGCTGAAACACGCCATCCGTGTCGAAATAA
Qy	421	GGAGATATGCTCAGTCGTCCTGCGAGATATCAGTCGTTGAAAGG
Db	1039	GGAGATATCTCAGTCGTCAGCGCGTACCTCTCGTGTGAAAGTAC
Qy	481	TGAGAGCTATGAGCGTGTGGCTGTTGAGTATCACCTCAGATCGGGT
Db	1059	TCTGAGACATGCAAAAGTGGCAAGACGGGTGTCACTCACCAGAGTC
Qy	541	ATGGAAACAGACTGAGTGTGAGCTGAGTCAGAATGTTGAGCTG
Db	1159	ATGGAAACAGACTGAGTGTGAGCTGAGTCAGAATGTTGAGCTG
Qy	601	TACATGGTCACAGCAATCAAAATGGTGTGAGACCTGTCAGTC
Db	1219	TACATGGTCACAGCAATCAAAATGGTGTGAGACCTGTCAGTC
Qy	661	ACGGATAAAAGGTCACACATTCCAGACATTGCCACTTCTGGAGTC
Db	1279	ACAGCAGCAGAAATTCAGATATCCAAAGAAATCTCCACTTGTGAAAGCATCTCCAA
Qy	721	ACCAACCTCTTACTATATTCAGATGTTGGATGGAAACACATCCT
Db	1339	ACGAACTCTCCCTTGTATTCAGATGTTGGATGGAAACACATCCT
Qy	781	TCTGAGACAAAGTTCGTTGACTCTCATGTTGTCAGTCAGTC
Db	1399	TCTTGTGACAAAGATTCGGAACTCTCACGTTGTCAGTCAGTC
Qy	841	TATGTCCTAAAGCTATGTCAGACACATTGTCAGTCAGTCAGTC
Db	1459	ACGGTGTGCAAGGCCATGCTTCAGATGTCAGTCAGTCAGTC
Qy	901	GAGGCTCTAGCTGTTGAAAGATCTACATGACAGCCTGTCAGTC
Db	1519	GAAGACCTGTCGTTGAAAGATCTACATGACAGCCTGTCAGTC
Qy	961	ATTACAGTTGATTAAGATAGACACTAATTTGTTGAGGTTCAGAGCTT
Db	1579	GTGACCTGGAAAGATAGTCAGCAGCTTATGTTAGAGGTTGAGGATT
Qy	1021	GCTAACCTTGTCACTGATTAATCGCAATAGAACACACTTCTGACTT
Db	1639	TCTACCGCTGTTGGGTATCAAGTCACATTGCAACTCTGCAATT
Qy	1081	GAAGACTACAGACGCTGGGAAATGACTGTTGAGGTTGACTCTT
Db	1699	GAAGAATGCAAGACGCTTGGCAATTGTCAGTGTGAGGTTAGGGT
Qy	1141	GCTCCAAAGAGACGCTTAAAGAATGAACTTCGATGAGTCCTAATGCT
Db	1759	GGCCCACTGTCAGTGTGAGAATGAAACCTCCGATGAGTCCTCAGCT
Qy	1201	ACAGCTGTCAGCGTGTGAGAAGGATCTCTGTTGAGACAGCACTT

Db 1819 ACGCGTGCACTGCTGAGAAGGGTTGGAGCTGGACACCTCTGCCAATG 1878
 Qy 1261 ATGGAAGAAAGTAGCAGCTCTGACTCTGGCGCTGTGACTGGAGTACATG 1220
 Db 1879 ATTCAGCTGAACTACTCTGGATTGAGCTGAGGAGTGAAGCACAGGAGTAAATG 1938
 Qy 1321 CTTCGGCTCTAAGAGCTGTCGAATGCTTAATGCTGCTGAGCTGGAGCTCC 1380
 Db 1939 ATTCAGCTGAACTACTCTGGATTGAGCTGAGGAGTGAAGCACAGGAGTAAATG 1938
 Qy 1381 GATGTTATTGACAGTGAAGAACAGCCCTGACGACAGGTTAACTGCAAC 1440
 Db 1999 ATTCAGCTGAACTACTCTGGATTGAGCTGAGGAGTGAAGCACAGGAGTAAATG 1440
 Qy 1441 GAGTGGTTGATGTTAAACGGATCTTGCCTGTCAAAGTAACTGAGTCAGCC 1500
 Db 2059 GATGTTATTGACAGTGAAGAACAGCCCTGACGACAGGTTAACTGCAAC 2118
 Qy 1501 CTCAAAATGCACTCTGTCAGTCAGCTTATTTGACACAGAACAGCAGTTCTG 1560
 Db 2119 CTACAAATGCACTCTGTCAGTCAGCTTATTTGACACAGAACAGCAGTTCTG 2178
 Qy 1561 AACCTGAAACCTAGCCAGGCCAGCANTGCCAGGATGTCAGGANTG 1620
 Db 2179 AACCTGAAACCTAGGCCAGCCTCCAGCATGGTACAGCAGTGGGGGATG 2238

RESULT 15

ABRA0521
 ID ABRA0521 standard; DNA; 2365589 BP.
 AC ABRA0521;
 XX
 DT 16-MAY-2002 (first entry)
 DE Genomic sequence of Lactococcus lactis I1403.
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.
 OS Lactococcus lactis I1403.
 XX
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PF 11-APR-2000; 2000FR-0004630.
 PR 11-APR-2000; 2000FR-0004630.
 XX
 (INRG) INRA INST INAT RECH AGRONOMIQUE.
 PT Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 DR WPI: 2002-04-3418/06.

PT New nucleotide sequence useful in the identification of Lactococcus
 lactis and related species -

XX
 Claim 1; SEQ ID 1; 250PP; French.

XX
 The present invention is related to a Lactococcus lactis nucleotide
 sequence (ABRA0521) and related proteins (ABR53100-ABR5621). The
 nucleic acid sequence is useful in the detection and/or amplification of
 nucleic acid sequence, particularly to identify Lactococcus lactis or
 related species. The proteins of the invention are useful for the
 biosynthesis or biodegradation of a composition of interest. The
 invention helps research in lactic bacteria, particularly useful in the
 production of yogurt and cheese.

CC Note: The sequence data for this patent is based on equivalent patent
 CC WO20017334 (published 18-OCT-2001) which is available in electronic
 CC format directly from WIPO at http://wipo.int/patents/pct_sequences.
 XX
 Sequence 2365589 BP: 765914 A; 415261 C; 420467 G; 763927 T; 0 other;

Query Match 58 3%; Score 954 2; DB 24; Length 2365589;
 Best Local Similarity 75.2%; Pred. No. 2.2e-38;
 Matches 1190; Conservative 0; Mismatches 393; Indels 0; Gaps 0;

Qy 1 ATGCCAAGAAATCAATTTCAGGAGTGGCGCTCCATGGCGGGAGTGT 60
 Db 398897 ATGCAAAAGATATTAATTTCACTGTTGAGCTGAGTCAGTGGCGGGAGTGT 398956
 Qy 61 ATGTTAGAGATACCGTCAAATTAAGCTGTTGTCAGGATTTGAGCTGAGTCAGTGGCGGGAGTGT 120
 Db 39857 ATTCAGCTGAACTACTCTGGATTGAGCTGAGGAGTGAAGCACAGGAGTAAATG 120
 Qy 121 AAAGCTTGGTCTCCCTTAATTAATGAGGGTTAACCTCTCTAAAGAGATGCAA 180
 Db 399017 AAATCTATGATCACCTTTAATTAATGAGGGTTAACCTCTAAAGATGCAA 399076
 Qy 181 TTAGAGTCATTGAAACATGGGAAATTTGGTCAGTAAAGGGCTTAAACC 240
 Db 399077 CTTCAGATGTCATTGAAATATGGAGGCTTAACCTGTTGAGCTAAGGGTTTAACC 399136
 Qy 241 AAATGATATGTTGGTGTGAGGACTGACTGCAACAGTTGACAGCATTGTCAGTAAAGGGCTTAAACC 300
 Db 399137 ATTCATATGGAGGTGACACACAGGGACAGTGTGACACAGCTATGTTG 399196
 Qy 301 GAAGACAAAGAAATGTCAGCAGTCATTCATGGTCAGTAAAGGGCTTAAACC 360
 Db 399197 GAAGGTTTAAATGTTAACCTGAGTGTGCAATCCCTGTTGCGAGGATGAA 399256
 Qy 361 ACACCAACAGAACAGCTGTTGAGGCTTGAAACCTGAGCTCACTGTTGCAAG 420
 Db 399257 CTTCAGCTGAAACAGCTGTTGAGGCTTGAACTTAAAGAGATGTCAGA 540
 Qy 421 GAAGCTTATGTCAGGTTGGCGCACTATCACCGCTGAAAGTTGGAGTATC 480
 Db 399317 TCAGCAATTGCGCAGTAGCTGTTACATCCTACTAGTAAAGTGGTGTAAAT 399376
 Qy 481 TCAGAGCTATGGAGCCTGGGGAAACCATGGTCGATTAACCATGAGACTTCAGGT 540
 Db 399377 TCTTCAGCTGAAATGGAGCTGTTGAGGCTTAAACCTGTTGCA 399316
 Qy 541 ATGCAACAGAACAGCTGTTGAGGTTGAGGCTTGCAATTCAGGATGTCAGA 600
 Db 399437 ATGCAACAGAACAGCTGTTGAGGCTTGAGGATGTCAGTGGTGTAAAT 399496
 Qy 601 TACATGTCAGCAGTAAAGTAAATGTTGAGCTGTTGAGGATGTCAGGATGTCAGTAAAT 660
 Db 399497 TATATGTTCTTAATACAGAAAAATGTTGAGTAAACCTTATTCCTAAAT 399556
 Qy 661 ACGGATAAAAGTGTAAACATCCAGCTTGGCAACTTGAGGTTGAGGATGTCAGTAAAT 720
 Db 399557 ACGGATAAAAGTGTAAACATCCAGCTTGGCAACTTGAGGTTGAGGATGTCAGTAAAT 399616
 Qy 721 ACCAACCGGCAATTACATCATGGAGCATGGATGGTGAAGCACTCCACCC 780
 Db 399617 ACACATGCGCACTCTCTTATGTTGAGCTGATGATGTTGAGGAGCATGTCACGCT 399676
 Qy 781 GCTTCACAGATCTGTTGACTTCACTGTTGAGGTTGAGGCTTGCAAGCCAGGATTG 840
 Db 399677 GTCCTAAAGTTAAAGTGTGCTCACTGTTGAGGTTGAGGAGCATGTCACGCT 399736
 Qy 841 GATCGTGTGAACTCTGTTGAGCATCTGTTGAGGTTGAGGAGCATGTCACGCT 399736
 Db 399737 GATCGTGTGAACTCTGTTGAGCATCTGTTGAGGTTGAGGAGCATGTCACGCT 399796
 Qy 901 GAGGATGAGCTGAGTGAATTAAGATGTCAGCAGTCAGGAGCTGGAGCAGCTTAAAG 960
 Db 399797 GAGGAGCTGTTGAGCTTAATGAGTGTGAGGTTGAGGAGCTGAGCAGCTTAAAG 399856
 Qy 961 ATTAGCTGAGTGAATGAGCTGAGTGTGAGGTTGAGGAGCTGAGCAGCTTAAAG 1020
 Db 399857 GAACTGTGAGTGAAGCAGCACACAGTGTGAGGTTGAGGTTGAGCTGAGCTTAAAG 399916

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QY 1021 GETAACCGTATGCACTGACTGTTAATGCGAAATTAGAACACACTCTGACTTTGACCGT 1080
 Db 399917 TCTGTGCTGCTGCTGTTTAAGCGAAATGCGAACTCTGACTGTTGACGT 399976
 QY 1081 GAAARACTACAGAACGTTGGAATTAGCTGTGTTGAGCTGTTGAGTGTGAAAGTGA 1140
 Db 399977 GAAATATTCAGAACGCTTGTGCGAAATTAGCTGTGTTGAGCTGTTGAAAGTGT 400036
 QY 1141 GCTCCAACGAGACACTTAAAGAAATGAACTTGGCAATTGCGATGCTAAAGCT 1200
 Db 400037 GCTGGCAGTGAACAGCTCAAGCATCAACTCTGTGAGATGACTTAATGCA 400096
 QY 1201 ACACCTGAGCGCTGAGAAGCTGAGCTGCTGCGCTGTTGAGCACGACTTAAAGCT 1260
 Db 400097 ACACCTGAGCGCTGAGAAGCTGAGCTGCTGCGCTGTTGAGCACGACTTAAAGCT 400156
 QY 1261 ATGAAAGAATGAGCTGAGCTGAGGGAGATCTGAGCTGAGCTGAGCTAATGCG 1320
 Db 400157 ATGGCTGCTGAGAACTTCAAGAGAGGAGGATTTCAACGCTTAACTGATTT 400216
 QY 1321 CTTCGCTCTGAGAGGCTGAGCTCAATGCTGTTAATGCTGGTACGAGCTGAGCT 1380
 Db 400217 GCGCTGCTGAGAACACTCTCCATATGCTGCCATGCGAGATGAGGCTCA 400276
 QY 1381 CTGTTATTGACAACTGAAACACGCCCTGCGAACAGGATTATGCTGCACGGT 1440
 Db 400277 GTTACATGATTAACCTCTGCTGAGAGGAGTGGTACGAGATTCATGTGCACTGT 400336
 QY 1441 GAGGGGGTGAATGATGTTAAACAGAACGAACTGACCCCTGCTCAAACGATGG 1500
 Db 400337 CAACTGGTAAATATGTTGAGAGGATGTTGACCTCACAAGTGAACGATGG 400396
 QY 1501 CTTCAAATGCGCTCTGCTACTCTTATTTACACACAAACGAGTGTGCTA 1550
 Db 400397 TTGCAACAGGGCTCTGCTGCTGGTAAATTGACTACTGAAAGTAGTGTCTAAT 400456
 QY 1561 AACCTGACCACTAACGCC 1583
 Db 400457 AACGCAGAACGCTGTCAGC 400479